

SEQUENCE LISTING

<110> Cahoon, Rebecca E..
Fang, Yiwen
Odell, Joan
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

<130> BB1294 US NA

<140>

<141>

<150> 60/110, 609
<151> 1998-December-02

<160> 63

<170> Microsoft Office 97

<210> 1
<211> 771
<212> DNA
<213> Zea mays

<220>

<221> unsure
<222> (4)

<220>

<221> unsure
<222> (99)

<220>

<221> unsure
<222> (396)

<220>

<221> unsure
<222> (470)

<220>

<221> unsure
<222> (486)

<220>

<221> unsure
<222> (586)

<220>

<221> unsure
<222> (600)

<220>

<221> unsure
<222> (612)

```

<220>
<221> unsure
<222> (615)

<220>
<221> unsure
<222> (627)

<220>
<221> unsure
<222> (632)

<220>
<221> unsure
<222> (658)

<220>
<221> unsure
<222> (690)

<220>
<221> unsure
<222> (716)

<220>
<221> unsure
<222> (724)

<220>
<221> unsure
<222> (736)

<220>
<221> unsure
<222> (752)

<220>
<221> unsure
<222> (758)

<400> 1
caancgcggg attgttcaat ccgttcgaca tcacaaaatc cacgcacaaa gaagcgacag 60
atgactacga gcaggggtggc caggtcgtgc ggccgcggna gcgacgatga gccggcggtg 120
cgcaaggggc cgtggacgct ggaggaggac ctcatcctcg tcagctacat ctcccagcac 180
ggggagggct cctggacaa cctcgcgcgc gcagctggac tgaaccgcaa cggcaagagc 240
tgcaggctgc ggtggctcaa ctacctgagg ccgggggtgc ggccgcgcag catcacggcg 300
ggggaggaca cggtcatccg ggagctccac gcgaggtggg ggaacaagtg gtccaagatc 360
tccaagcacc tccccggccg aaccgacaac gagatnaaga actactggag gaccaggatc 420
caacaagaag aacagaagg agccaagacg acgcaacaac gggaccgtcn acgaccgcca 480
actccngggc ccggggacga ctactgggtg cacaacccga ccccgacaac aagccatact 540
gcctgcaaaa accccatgca actgcacgctg acaacaacccg gtctcnataac aacaagacan 600
ccccttcggg gnctnacaac cagaaanccc cnccggcggg gaatggtaat cacaacanaa 660
attgtaccct ctgtccaact aactttcccn cggcacataa acgtcggtcg accttnacaa 720
tcantttctt ccaactnatgc actttgcaac gngtgtantt tgataaaacct t 771

<210> 2
<211> 157
<212> PRT
<213> Zea mays

```

<220>
 <221> UNSURE
 <222> (111)

<220>
 <221> UNSURE
 <222> (136)

<400> 2
 Thr Thr Ser Arg Val Ala Arg Ser Cys Gly Arg Gly Ser Asp Asp Glu
 1 5 10 15
 Pro Ala Val Arg Lys Gly Pro Trp Thr Leu Glu Glu Asp Leu Ile Leu
 20 25 30
 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala
 35 40 45
 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60
 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly
 65 70 75 80
 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp
 85 90 95
 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys
 100 105 110
 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys
 115 120 125
 Thr Thr Gln Gln Arg Asp Arg Xaa Arg Pro Pro Thr Pro Gly Pro Gly
 130 135 140
 Asp Asp Tyr Trp Val His Asn Pro Thr Pro Thr Thr Ser
 145 150 155

<210> 3
 <211> 782
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (3)

<400> 3
 acngtctgct gcaggtacgg gccgtaatcc gggtcgacca cgcgtccccga caaagtggca 60
 tactttctc tgtactagct ttctttttcc tctcctcttc ctcacaaaca gactggattt 120
 caacaagata atcctgaaac tggagccaaac aagcacacag agaaaagaaga gcaagaagac 180
 cggctcccaag ccgatatacaag ttaggaggatga gcagcgtag tttcatcata tcgcataaggc 240
 gatatggtga cagttagaaaa ggagactcgc aaggggccat ggacagagca ggaggacctg 300
 caactggtat gcactgtccg tctgttcggt gaacgtcggt gggatttcat tgccaaagta 360
 tcaggactca accggacagg caagagctgc cggctgcgggt gggtaacta cctccaccct 420
 ggcctcaagc gtggggcat gtctcccat gaagagcgcc tcatccttga gctgcacgct 480
 cggtggggaa acaggtggtc caggatagca cggcgcttgc cagggcgcac tgacaatgag 540
 atcaagaact actggaggac acacatgagg aagaaaagcac aggagaggaa gaggaacatg 600
 tctccatcatc catcctcattc ttcaactgagt taccagtcag gctaccaga taactccatca 660

atcattggag ttaaggaca ggagcttcat ggtggcagtg gctgcacac aagcatcctg 720
aaggccaccc atccggacat ggatggctat cccatggacc agatatggat ggaattgaag 780
gg 782

<210> 4
<211> 179
<212> PRT
<213> Zea mays

<400> 4
Met Val Thr Val Arg Glu Glu Thr Arg Lys Gly Pro Trp Thr Glu Gln
1 5 10 15

Glu Asp Leu Gln Leu Val Cys Thr Val Arg Leu Phe Gly Glu Arg Arg
20 25 30

Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser
35 40 45

Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly
50 55 60

Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg
65 70 75 80

Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr
85 90 95

Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala
100 105 110

Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Leu
115 120 125

Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys
130 135 140

Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys
145 150 155 160

Gly Thr His Pro Asp Met Asp Gly Tyr Pro Met Asp Gln Ile Trp Met
165 170 175

Glu Leu Lys

<210> 5
<211> 601
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (451)

<220>
<221> unsure
<222> (456)

<220>
<221> unsure
<222> (478)

<220>
<221> unsure
<222> (480)

<220>
<221> unsure
<222> (490)

<220>
<221> unsure
<222> (510)

<220>
<221> unsure
<222> (542)

<220>
<221> unsure
<222> (549)

<220>
<221> unsure
<222> (552)

<220>
<221> unsure
<222> (554)

<220>
<221> unsure
<222> (572)

<220>
<221> unsure
<222> (578)

<220>
<221> unsure
<222> (583)

<220>
<221> unsure
<222> (588)

<220>
<221> unsure
<222> (595)

<220>
<221> unsure
<222> (601)

<400> 5
aaccggccat catcggttat acctaccagc tcgctgttct tgctgaagcc ctggagctat 60
atagcttcga tctgcgcagc acagggttgtc tgtcgacttag tgatttagtga agaagatggc 120
ggcgcgtgac caccgagagc tgagcggcga cgaggactcc gtgggtggcgg ccggagacct 180

ccggccgcggg ccgtggacgg tggaggagga catgctcctc gtcaactacg tcgcccgcga 240
cgcgaggggc cgcttggaaacg cgctggcacg atgcgcaggg ctccggcga cggggaaagag 300
ctgccgcctg cggttggctca actacctgcg gccggacctg cggcggggca acatcacggc 360
gcaagagcaa ctgctcatcc tggagctgca ctccccgtgg ggcaaccgct ggtcaagatc 420
gcccagcacc tccaaggggca acgacaaacga natcanaact actggcgcac cggttcanan 480
caccagcan ctcaatgcaa ctcaaagcan cgctcaagga ctcagcgcta atctggatgc 540
ngngctccna angnaccgtc gacatccggg angggctnct ttngagcnca cccancaaac 600
n 601

<210> 6
<211> 120
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (101)

<220>
<221> UNSURE
<222> (113)..(114)

<400> 6
Met Ala Ala Arg Asp His Arg Glu Leu Ser Gly Asp Glu Asp Ser Val
1 5 10 15

Val Ala Ala Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp
20 25 30

Met Leu Leu Val Asn Tyr Val Ala Ala His Gly Glu Gly Arg Trp Asn
35 40 45

Ala Leu Ala Arg Cys Ala Gly Leu Arg Arg Thr Gly Lys Ser Cys Arg
50 55 60

Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile
65 70 75 80

Thr Ala Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly
85 90 95

Asn Arg Trp Ser Xaa Ile Ala Gln His Leu Gln Gly Gln Arg Gln Arg
100 105 110

Xaa Xaa Asn Tyr Trp Arg Thr Gly
115 120

<210> 7
<211> 547
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (356)

<220>
<221> unsure
<222> (374)

```

<220>
<221> unsure
<222> (479)

<220>
<221> unsure
<222> (508)

<220>
<221> unsure
<222> (532)

<400> 7
ccgataaccgg cctcaacgcc ctcttttcc cagcctcaca accaattcct gtttcagtcg 60
atcgcatgtt gcatggccac gacacagagc tgcagagca ggagcagcgc ctgcagcaag 120
gctgtgtt gctccggc cgccgttagcg gtcgacgagg agcacggcca ccacagccac 180
cagctgaagg gaggagcgca ggaggaggct gagaacgaca ataataagcc ggagctccgg 240
cgtggccctt ggacggtaga cgaggacactc accctcgta actacatcgc cgacaacgac 300
gagggtccctt ggaacaacctt cgcccgccgccc gccgggctga agcggacggg caaganctgc 360
cggctgcgtt ggcncaacta cttccggccc gacgtgaagc gtggaaactt cagcgccgac 420
gagcagtcgac tcatctcgac ctcacaccgc tggggcaacc gatgtcgaag atagcgcanc 480
acctgccggg aaggacggca acgagatnaa gaactactgg aggaccgggt gnataacacg 540
caagatc 547

<210> 8
<211> 72
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (42)

<220>
<221> UNSURE
<222> (48)

<400> 8
Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Val
    1           5           10          15

Asn Tyr Ile Ala Asp Asn Gly Glu Gly Pro Trp Asn Asn Leu Ala Arg
    20          25          30

Ala Ala Gly Leu Lys Arg Thr Gly Lys Xaa Cys Arg Leu Arg Trp Xaa
    35          40          45

Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu
    50          55          60

Gln Leu Leu Ile Ser Thr Ser His
    65          70

<210> 9
<211> 1317
<212> DNA
<213> Zea mays

```

<400> 9

```

gcacgagccg ataccggcct caacgcctc ttttcccag cctcacaacc aattcctgtt      60
tcagtcgatc gcaggtagca tggccacgac acagagctgt cagaggcaga gcagcgctg     120
cagcaaggct gctgcttgct tcccggccgc cgtagcggtc gacgaggagc acggccacca    180
cagccaccag ctgaagggag gagcgcagga ggaggctgag aacgacaata ataagccgga   240
gctccggcgt gccccctgga cggtagacga ggacctcacc ctcgtcaact acatcgccga  300
caacggcgag ggtcgctgga acaacctcgc ccgcgcgc gggctgaagc ggacgggcaa  360
gagctgccgg ctgcggatgc tcaactacct ccggcccgac gtgaagcgtg gcaacttcag  420
cgccgacgag cagctgctca tcctcgaccc ccacacccgc tggggcaacc gatggtcgaa  480
gatagcgcag cacctgcccgg gaaggacgga caacgagatc aagaactact ggaggacccg 540
ggcgcagaag cacgccaagc agctcaactg cgacgccaac agcaagcgtc tcaaggacgc 600
catgcgtac ctctggatgc cgcacctcgc cgacgacgac gataccatcg ctgcggccaa 660
cgacgacgac gaagaccacc accacaacct acgcctcgc gtcctgcacc accaccagc 720
ccagcacctg cagcaagctg ctggcgccgc cggcgccgct gccaacgacc ttgctgcggg 780
cgccctacgac gtccgcccgc tgacgcgcgct gccgtcgctg ggcattggcg cgacgtcgctc 840
gtccgactcg ctcgcgtcg agtgcgtacga tgacggaggc ctgcgtttcg cgaacttgcg 900
cgccggcgag atgctgatgg acggcggaga ttggggccgc cagcaggagg cgcaccaagg 960
gctgtggccg cgcgcgcgc cgccgcgc tgatcttgat cagtcgggtgg tgcaggctgc 1020
tggtgccggc gctggccagt ttcaggacat ggagctcagt ggttgggtgc aaggcttctc 1080
cgagagcatt acagataact tttgggcctt ggaggaaatt tggaaagatgc aatgagcgg 1140
caattttaca tcttacacat ccattccaaat taaagacaac atagatacac atatacatat 1200
catatattct aacaacaggt gccatatacg atatacatac acaagttgtt gtatagttgt 1260
attccgctta tatatatatt tttttgcct ctcaaaaaaaaaaaaaaaa aaaaaaaaaa 1317

```

<210> 10
<211> 351
<212> PRT
<213> Zea mays

<400> 10

Met	Ala	Thr	Thr	Gln	Ser	Cys	Gln	Ser	Arg	Ser	Ser	Ala	Cys	Ser	Lys
1															
				5					10						15

Ala	Ala	Ala	Cys	Phe	Pro	Ala	Ala	Val	Ala	Val	Asp	Glu	Glu	His	Gly
				20				25							30

His	His	Ser	His	Gln	Leu	Lys	Gly	Gly	Ala	Gln	Glu	Glu	Ala	Glu	Asn
				35			40								45

Asp	Asn	Asn	Lys	Pro	Glu	Leu	Arg	Arg	Gly	Pro	Trp	Thr	Val	Asp	Glu
				50			55								60

Asp	Leu	Thr	Leu	Val	Asn	Tyr	Ile	Ala	Asp	Asn	Gly	Glu	Gly	Arg	Trp
				65		70			75						80

Asn	Asn	Leu	Ala	Arg	Ala	Ala	Gly	Leu	Lys	Arg	Thr	Gly	Lys	Ser	Cys
				85			90								95

Arg	Leu	Arg	Trp	Leu	Asn	Tyr	Leu	Arg	Pro	Asp	Val	Lys	Arg	Gly	Asn
				100			105								110

Phe	Ser	Ala	Asp	Glu	Gln	Leu	Leu	Ile	Leu	Asp	Leu	His	Thr	Arg	Trp
				115			120								125

Gly	Asn	Arg	Trp	Ser	Lys	Ile	Ala	Gln	His	Leu	Pro	Gly	Arg	Thr	Asp
				130			135			140					

Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Arg	Thr	Arg	Val	Gln	Lys	His	Ala	Lys
				145			150			155					160

Gln Leu Asn Cys Asp Ala Asn Ser Lys Arg Phe Lys Asp Ala Met Arg
 165 170 175

Tyr Leu Trp Met Pro His Leu Ala Asp Asp Val Asp Thr Ile Ala Ala
 180 185 190

Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val
 195 200 205

Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala
 210 215 220

Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln
 225 230 235 240

Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp
 245 250 255

Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn
 260 265 270

Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln
 275 280 285

Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser
 290 295 300

Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln
 305 310 315 320

Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser
 325 330 335

Ile Thr Asp Asn Phe Trp Ala Leu Glu Glu Ile Trp Lys Met Gln
 340 345 350

<210> 11
 <211> 488
 <212> DNA
 <213> Oryza sativa

<400> 11
 ggttcgtgcg gctgctggc gaacggcggt gggatttctt agcaaagggtc tcaggtttgc 60
 gcggccggcg gtgatgagca tatgcgtgcg tgcataat ctatcgatta attgttgatg 120
 atgtcgatca gatggatgga tgcatacgata tgccgtacat agtagatttg atgatagtaa 180
 ctgacataaa tataatgtat gcgtgcgatc aacgctgggtt gttggatcgt ccgtcgtgtg 240
 tatgggtgggtt gtgtggctga tgcagggttg cagcgcagcg ggaagagctg ccgtctccgg 300
 tgggtgaact acctgcattcc agggctgaag cgagggagga tgagccccga ggaggagagg 360
 atggtgtgtgc agctccacgc caagctggc aacaggttgtt ctcgcattcc caagagcatt 420
 cctggccgca ccgacaacgca gatcaagaac tactggcgca cccacctgctgca caagctcaag 480
 ctcaaaca 488

<210> 12
 <211> 71
 <212> PRT
 <213> Oryza sativa

<400> 12
 Val Tyr Gly Trp Cys Val Ala Asp Ala Gly Leu Gln Arg Ser Gly Lys
 1 5 10 15

Ser Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg
20 25 30

Gly Arg Met Ser Pro Glu Glu Arg Met Val Val Gln Leu His Ala
35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg
50 55 60

Thr Asp Asn Glu Ile Lys Asn
65 70

<210> 13
<211> 1123
<212> DNA
<213> Oryza sativa

<400> 13
gcattcttt tctgcatcat catcgtcgtc ttctgttct tcttggtag tagtgcagct 60
gggtcatcat cagcgccac agggtgagga ccctctcatc ggcataaaag cagcagcagc 120
aggaggagga ggaataatga gaaagggccc gtggacggag caggaggacg tgcaagggtt 180
ttgggtcggt cggtcgctgg gcgaacggcg gtgggatttc ttagcaaagg tgtcagggtt 240
gcagcgcagc gggaaagagct gccgtctccg gtgggtgaac tacctgcatac cagggctgaa 300
gcgaggaggagg atgagccccg aggaggagag gatgggtggtg cagctccacg ccaagctcgg 360
caacaggtgg tctcgcatcg ccaagagcat tcctggccgc accgacaacg agatcaagaa 420
ctactggcgc acccacctgc gcaagctcaa gctaaacacg caaaaacgc agcagtccga 480
cgaccaccac aacgacaacg acgacgacga cgaccgcaac tcctccctt ctgcgtcctc 540
ctccaacacgc aacagcaacc tgcagcagca gcccgcacca gaggatgagt cgtcgccag 600
tggcagcctg caggcccaac atcatgagga ccagcaccaa ctgttccttc atcctctctg 660
gaacgacgac atcatcgatcg acgtcgactg ctggagcagc agcacaacg tcgtcgctcc 720
gccgcccgtat cccgcctcgc cgctctggta tatcgatgac gccttcttct gtcggattta 780
ttcgctacct ctctgggat agtatataatc atccatcagc cgccaaagacg atgacgacta 840
catcaactcg atcgatcgat gcctccta atcatgatcg tactcagctc atctcaattt 900
ttacatcctt gctacagctg ctaattactg taattactg ctgcataata gggatcgacg 960
gaggaattaa tatatacatg ttagtaactc gttctatagc gcaacttgca gttgcatactc 1020
aatctctgtat cagtactata taaatatata tatatatgtt acagctgcta gctatagcta 1080
gctgcgtaca catccatatg aatgtgtgtg tgttcatgct aaa 1123

<210> 14
<211> 221
<212> PRT
<213> Oryza sativa

<400> 14
Met Arg Lys Gly Pro Trp Thr Glu Gln Glu Asp Val Gln Leu Val Trp
1 5 10 15

Phe Val Arg Leu Leu Gly Glu Arg Arg Trp Asp Phe Leu Ala Lys Val
20 25 30

Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
35 40 45

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu
50 55 60

Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg
65 70 75 80

Ile Ala Lys Ser Ile Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 85 90 95

 Trp Arg Thr His Leu Arg Lys Leu Lys Leu Lys Gln Gln Lys Gln Gln
 100 105 110

 Gln Ser Asp Asp His His Asn Asp Asn Asp Asp Asp Asp Arg Asn
 115 120 125

 Ser Ser Ser Ser Ser Ser Asn Ser Asn Ser Asn Leu Gln Gln
 130 135 140

 Gln Pro Gln Pro Glu Asp Glu Ser Ser Ala Ser Gly Ser Leu Gln Ala
 145 150 155 160

 Gln His His Glu Asp Gln His Gln Leu Phe Leu His Pro Leu Trp Asn
 165 170 175

 Asp Asp Ile Ile Val Asp Val Asp Cys Trp Ser Ser Ser Thr Asn Val
 180 185 190

 Val Ala Pro Pro Pro Met Pro Ala Ser Pro Leu Trp Asp Ile Asp Asp
 195 200 205

 Ala Phe Phe Cys Ser Asp Tyr Ser Leu Pro Leu Trp Gly
 210 215 220

 <210> 15
 <211> 336
 <212> DNA
 <213> Oryza sativa

 <220>
 <221> unsure
 <222> (308)

 <400> 15
 tctggagttg atcaaggctc taaacgtgaa gctggagcca acaaactcaa agaggaagaa 60
 gAACACGGAG agtggctccc atcctatcca aggttaagaag tgaacaacgt tagcattgca 120
 acatcccaag ccccaatatg gtgacagtga gagaggagat ggcgaaggga ccatggacag 180
 agcaggagga cctgcaactg gtatgcactg tccgcctgtt cggtgaccgc cggtgggatt 240
 tcgttgccaa agtatcaggt ttgagggggc tcaataggac aggcaagagc tgccgcctcc 300
 gttggtnaa ctaactccaa ccctgggcct caagca 336

 <210> 16
 <211> 62
 <212> PRT
 <213> Oryza sativa

 <220>
 <221> UNSURE
 <222> (59)

 <400> 16
 Met Val Thr Val Arg Glu Glu Met Arg Lys Gly Pro Trp Thr Glu Gln
 1 5 10 15

 Glu Asp Leu Gln Leu Val Cys Thr Val Arg Leu Phe Gly Asp Arg Arg
 20 25 30

Trp Asp Phe Val Ala Lys Val Ser Gly Leu Arg Gly Leu Asn Arg Thr
35 40 45

Gly Lys Ser Cys Arg Leu Arg Trp Val Asn Xaa Leu Gln Pro
50 55 60

<210> 17
<211> 587
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (577)

<220>
<221> unsure
<222> (582)..(583)

<220>
<221> unsure
<222> (587)

<400> 17
ctctactaca cacttgctct gcccgtatgat gatggcgca gaggtgagca gcgaggagga 60
ggctggcgcc ggcgacgagc tccggcgagg gccgtggacg gtggaggagg acctgctct 120
cgtcaactac atcgccgccc atggcgaggg cgcgtggaaac gcgctcgccg cgtgcgccgg 180
gctgaagcgg acgggaaaga gctgcccggct gcggtggctg aactacctga ggccggacgt 240
gaggaggggg aacatgacgg cggaggagca gctgctgata ctggagctcc atgggcggtg 300
gggaaatcggt tggagcaaga tcgcgcagca tctccccggc cgccaccgaca acgagatcaa 360
gaactactgg cgaccccgcc tccagaagca cgccaaggcac ctcaactgcg acgtcaactc 420
ccagcagttc aaggacctca tgcgctacct ctggatgccc gcctccctcga acgcatcaac 480
gctcctccca atccaatcca cgaccggacg acccgactct cgtctccgccc gcacactgat 540
cactcgactc tctcacgcca taacgcccgt cgcatgnca annacan 587

<210> 18
<211> 145
<212> PRT
<213> Oryza sativa

<400> 18
Met Met Met Ala Arg Glu Val Ser Ser Glu Glu Glu Ala Gly Gly Gly
1 5 10 15

Asp Glu Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu Leu
20 25 30

Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala
35 40 45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu
65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp
85 90 95

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
 100 105 110
 Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys
 115 120 125
 Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met
 130 135 140
 Pro
 145
 <210> 19
 <211> 440
 <212> DNA
 <213> Oryza sativa
 <400> 19
 gccggccgggtc tgaaggaggac tgggaagagc tgccggctcc ggtggctgaa ctatctccgg 60
 cccggatgtga agcgcggcaa cttcacccca gaggagcagc tgctcatcct cgacccctcac 120
 tccccatgggg gcaaccgatg gtccaaagata gcacaacatt tgcctggag gaccgacgac 180
 gagatcaaga actactggag gaccagagtg caaaagcatg ccaagcaact caatttgtat 240
 gtcaacagca agaggttcaa ggatgccatg aagtacctat ggatgcctcg cttgcccag 300
 cgcacatccatg ccagggctgg cgctgttat gatacgccag actacagcaa caacgactta 360
 tcatgtgtat ctggtgtaac aatggccact gttgctaatt gttttgatgg ctctccgagc 420
 atgggtacta gtcatccctc 440
 <210> 20
 <211> 146
 <212> PRT
 <213> Oryza sativa
 <400> 20
 Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
 1 5 10 15
 Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Thr Ala Glu Glu
 20 25 30
 Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser
 35 40 45
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn
 50 55 60
 Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp
 65 70 75 80
 Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro
 85 90 95
 Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser
 100 105 110
 Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met
 115 120 125
 Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser
 130 135 140

Ser Ser
 145

<210> 21
 <211> 640
 <212> DNA
 <213> Oryza sativa

<220>
 <221> unsure
 <222> (355)

<220>
 <221> unsure
 <222> (498)

<220>
 <221> unsure
 <222> (534)

<220>
 <221> unsure
 <222> (543)

<220>
 <221> unsure
 <222> (582)

<220>
 <221> unsure
 <222> (597)

<220>
 <221> unsure
 <222> (606)

<220>
 <221> unsure
 <222> (619)

<220>
 <221> unsure
 <222> (634)

<400> 21
 ggcgtacatc catccatcca tccatctatac cagagagcac agcaacggcg catatatagt 60
 acccctctac caaacacaaa caaccagaat ctcctgagct cgatctagct actagcttga 120
 tctatccat caatcgactg gcccgcgagg atcgatcgag actcgaaagg gagggatttt 180
 gatccggatc ggtcgacgat ggacatggcg cacgagaggg acgcgagcag cgaggaggag 240
 gtgatggcg ggcacactgc tcgcggccg tggacggtgg aggaggacct cctgctcgtc 300
 aactacatcg ccgcgcacgg cgaggccgc tggaaactcgc tcgcccgtc agcanggctg 360
 aaacgcacag gcaagagctg cccgctccgg tggctgaact acctccgtcc cgacccctccgg 420
 cgaggcaaca tcacggcga agagcagctg ctcatcctgg agctgcactc gcgggtgggaa 480
 aaccgctggt ccaagatngc gcagcaccctc ccggaaagca ccgacaacga gatnaagaat 540
 acnggcgcac gcgggtgcaga agcaccctaag cagtcaagtgc cnactcaaca gcaacantta 600
 aggacncatg cgctactcng gatccccgt cttnagggat 640

<210> 22
 <211> 115

<212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (53)

<220>
 <221> UNSURE
 <222> (100)

<220>
 <221> UNSURE
 <222> (112)

<400> 22
 Met Asp Met Ala His Glu Arg Asp Ala Ser Ser Glu Glu Glu Val Met
 1 5 10 15

Gly Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu
 20 25 30

Leu Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ser Leu
 35 40 45

Ala Arg Ser Ala Xaa Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
 50 55 60

Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile Thr Pro
 65 70 75 80

Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg
 85 90 95

Trp Ser Lys Xaa Ala Gln His Leu Pro Gly Ser Thr Asp Asn Glu Xaa
 100 105 110

Lys Asn Thr
 115

<210> 23
 <211> 484
 <212> DNA
 <213> Oryza sativa

<220>
 <221> unsure
 <222> (118)

<220>
 <221> unsure
 <222> (298)

<220>
 <221> unsure
 <222> (355)..(356)

<220>
 <221> unsure
 <222> (374)

```

<220>
<221> unsure
<222> (376)

<220>
<221> unsure
<222> (381)

<220>
<221> unsure
<222> (386)

<220>
<221> unsure
<222> (393)

<220>
<221> unsure
<222> (408)..(409)

<220>
<221> unsure
<222> (417)

<220>
<221> unsure
<222> (432)

<220>
<221> unsure
<222> (453)

<220>
<221> unsure
<222> (466)

<220>
<221> unsure
<222> (469)

<220>
<221> unsure
<222> (476)..(477)

<400> 23
cttacacacgt atcgagatcg agtagtagtg acacgcatac accaccaacc accgcccggcc 60
gccggccggcg agctgcagga tggggaggcc gccgtgctgc gacaaggctcg gggtgaanaa 120
ggggccatgg acgccccggagg aggacactgt gctggcttc tacatccagg agcacggcg 180
cgcaactgg cgccgggtgc cgacgaacac cgggctgtatcg ttgcagca agagctgcgg 240
gctccgggtgg acgaactacc tcaggccggg gatcaagcgg gggacttca ccgagcanga 300
ggagaagctc atcggttccacc tccaggctct cctcgcaac cggggggcaa cgatnnncgtc 360
gtacttgccg gganangacg ncaacnacat cangaatact gggAACANNc acctcangaa 420
gaactcaaga anatgcaagc caccggaggt ggnngaaaaca gcgcgnnc tcgganngtt 480
gcgg 484

<210> 24
<211> 126
<212> PRT
<213> Oryza sativa

```

<220>
 <221> UNSURE
 <222> (13)

 <220>
 <221> UNSURE
 <222> (73)

 <220>
 <221> UNSURE
 <222> (92) .. (93)

 <220>
 <221> UNSURE
 <222> (99)

 <220>
 <221> UNSURE
 <222> (101)

 <220>
 <221> UNSURE
 <222> (103)

 <220>
 <221> UNSURE
 <222> (105)

 <220>
 <221> UNSURE
 <222> (110)

 <220>
 <221> UNSURE
 <222> (113)

 <220>
 <221> UNSURE
 <222> (118)

 <220>
 <221> UNSURE
 <222> (125)

 <400> 24
 Met Gly Arg Pro Pro Cys Cys Asp Lys Val Gly Val Xaa Lys Gly Pro
 1 5 10 15

 Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
 20 25 30

 Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
 35 40 45

 Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

 Ile Lys Arg Gly Asn Phe Thr Glu Xaa Glu Glu Lys Leu Ile Val His
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Thr Xaa Xaa Ser Tyr Leu
85 90 95

Pro Gly Xaa Asp Xaa Asn Xaa Ile Xaa Asn Thr Gly Asn Xaa His Leu
100 105 110

Xaa Lys Asn Ser Arg Xaa Cys Lys Pro Pro Glu Val Xaa Lys
115 120 125

<210> 25

<211> 1427

<212> DNA

<213> Oryza sativa

<400> 25

gcacgagctt acacctgatc gagatcgagt agtagtgaca cgcatacacc accaaccacc 60
gccggccgccc gccggcgagc tgcaggatgg ggaggccgccc gtgtcgac aaggctcgcccc 120
tgaagaaggg gccatggacg ccggaggagg acctgatgct ggtctctac atccaggagc 180
acggcgccgg caactggcgc gccgtgcccga cgaacaccgg gctgatgcgt tgccagcaaga 240
gctgcccggct ccgggtggacg aactaccta ggccggggat caagcgggggg aacttcaccgg 300
agcaggagga gaagctcatc gtccacctcc aggctctcct cggcaaccgg tgggcagcga 360
tagcgtcgta cttggccggag aggacggaca acgacatcaa gaactactgg aacacgcacc 420
tcaagaagaa gctcaagaag atgcaggccg ccggaggtgg ggaagacagc ggcggccgcct 480
cgaggaggctt cggcgccgc ggcgacggcg acggcggcg gaaaagcgtg aaggccgccc 540
cacctaaggg gcagtggggag cggcggtgc agacggacat ccacacggcg cggcaggcgc 600
tgcgcgacgc gctctcgctc gaccaccccg acccgtcgcc ggcgacggcg gcggcggccgg 660
cgacgcccagc ggggtcgctc gccggcgta cggtcgagcgc ggacaacatc ggcggcgtgc 720
tgcagggtct gatgcgccc ggcggcgccg gcggcggccaa cggcaaggcc cccgaggcgt 780
cggggtcgac ctccacgacg ggcgacgc acgacggacg cgcgtctcc ggcgaggccg 840
cgccatccgc gtcccggtcg gcgagccaga gcggcggccgc cgccggccgc actgcccaga 900
cgccggagtg ctcgacggag acgagcaaga tggccaccgg cggcggccgc ggcggccccc 960
cgccggcggtt ctcgatgctg gagagctggc tgctcgacga cggcggcatg gggctcatgg 1020
acgtggtgcc attgggggac cccagttagt tcttttaagt gtatgataac caaaattaaa 1080
ttaatcaagt agacagcaag aacaaaaaaaaa aataatggaa agttggcgag ttaattaatc 1140
aagatgcaac taatcaaagc taattaaaag ggcttcgagt taatttcgg tgatttaat 1200
cgagtttgca ggtgttgatc tagcttggtt aattaatcct ttctttgtt gtttttagt 1260
taatttagtct ctctgtatgat gctagggttt ggaactgatc atatgtaaatg ttaatttataac 1320
taatggtagg cctgtgactt gtgatttagt agtcctgagt ggataaataa agacataaat 1380
gtacatctt ttaaaaagata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1427

<210> 26

<211> 323

<212> PRT

<213> Oryza sativa

<400> 26

Met Gly Arg Pro Pro Cys Cys Asp Lys Val Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
20 25 30

Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Gln	Glu	Glu	Lys	Leu	Ile	Val	His
65					70				75					80	
Leu	Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Ala	Ile	Ala	Ser	Tyr	Leu
	85							90						95	
Pro	Glu	Arg	Thr	Asp	Asn	Asp	Ile	Lys	Asn	Tyr	Trp	Asn	Thr	His	Leu
	100						105						110		
Lys	Lys	Lys	Leu	Lys	Met	Gln	Ala	Ala	Gly	Gly	Gly	Glu	Asp	Ser	
	115					120						125			
Gly	Ala	Ala	Ser	Glu	Gly	Gly	Gly	Arg	Gly	Asp	Gly	Asp	Gly	Gly	
	130				135				140						
Gly	Lys	Ser	Val	Lys	Ala	Ala	Ala	Pro	Lys	Gly	Gln	Trp	Glu	Arg	Arg
	145					150				155				160	
Leu	Gln	Thr	Asp	Ile	His	Thr	Ala	Arg	Gln	Ala	Leu	Arg	Asp	Ala	Leu
							165		170				175		
Ser	Leu	Asp	His	Pro	Asp	Pro	Ser	Pro	Ala	Thr	Ala	Ala	Ala	Ala	
							180		185				190		
Thr	Pro	Ala	Gly	Ser	Ser	Ala	Ala	Tyr	Ala	Ser	Ser	Ala	Asp	Asn	Ile
							195		200				205		
Ala	Arg	Leu	Leu	Gln	Gly	Trp	Met	Arg	Pro	Gly	Gly	Gly	Gly	Gly	
	210					215					220				
Asn	Gly	Lys	Gly	Pro	Glu	Ala	Ser	Gly	Ser	Thr	Ser	Thr	Thr	Ala	Thr
	225					230				235				240	
Thr	Gln	Gln	Gln	Pro	Gln	Cys	Ser	Gly	Glu	Gly	Ala	Ala	Ser	Ala	Ser
						245			250				255		
Ala	Ser	Ala	Ser	Gln	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Thr	Ala	Gln	Thr
							260		265				270		
Pro	Glu	Cys	Ser	Thr	Glu	Thr	Ser	Lys	Met	Ala	Thr	Gly	Gly	Ala	
							275		280				285		
Gly	Gly	Pro	Ala	Pro	Ala	Phe	Ser	Met	Leu	Glu	Ser	Trp	Leu	Leu	Asp
						290		295				300			
Asp	Gly	Gly	Met	Gly	Leu	Met	Asp	Val	Val	Pro	Leu	Gly	Asp	Pro	Ser
	305					310				315				320	
Glu	Phe	Phe													

<210> 27
<211> 557
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (136)

<220>
<221> unsure
<222> (229)

<220>
<221> unsure
<222> (271)

<220>
<221> unsure
<222> (373)

<220>
<221> unsure
<222> (382)

<220>
<221> unsure
<222> (386)

<220>
<221> unsure
<222> (424)

<220>
<221> unsure
<222> (475)

<220>
<221> unsure
<222> (493) .. (494)

<220>
<221> unsure
<222> (511)

<220>
<221> unsure
<222> (520)

<220>
<221> unsure
<222> (522)

<220>
<221> unsure
<222> (531)

<220>
<221> unsure
<222> (536)

<220>
<221> unsure
<222> (552) .. (553)

<400> 27
tctctctccc ctctccccca cccaaccttc tctctatcac acacacaaaaa caatggataa 60
aaaacaactg tgcaacacgt ctcaagatcc tgaagtgaga aaaggacctt ggacgatgga 120
agaagacttg atcttngatc aactatatgg caaatcatgg ggaagggtgtt tgaattctt 180

tggccaaaag ctgctggtct caaacgtacc ggaaagattt ccggctaang tggctaaact 240
acctccgtcc tgatgttaga agagggata ntacacccga aggaacaact ttgatcatgg 300
agcttcacgc aaagtggga aacaggttgtt ccaaaaattgc caagcatcta cctggtagga 360
cagtaatgag atnaagaact antggngac aaggatcaga agcacatcaa gcaactgaga 420
attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480
gttgaaccat ggnactatc ccaaccttt naaggaagtn angcatttct naatcntcc 540
ccaaataacc gnntatc 557

<210> 28
<211> 94
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (19)...(20)

<220>
<221> UNSURE
<222> (51)

<220>
<221> UNSURE
<222> (65)

<400> 28
Ser Gln Asp Pro Glu Val Arg Lys Gly Pro Trp Thr Met Glu Glu Asp
1 5 10 15

Leu Ile Xaa Xaa Ile Asn Tyr Ile Ala Asn His Gly Glu Gly Val Trp
20 25 30

Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys
35 40 45

Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn
50 55 60

Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp
65 70 75 80

Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr
85 90

<210> 29
<211> 988
<212> DNA
<213> Glycine max

<400> 29
cgcacgagtc tctctcccct cttccccacc caacccatctc tctatcacac acacaaaaaca 60
atggataaaaa aacaactgtg caacacgtct caagatcctg aagtgagaaa aggaccttgg 120
acgatggaaag aagacttgat cttgatcaac tatattgcaa atcatggggaa aggtgtttgg 180
aattctttgg ccaaagctgc tggctctaaa cgtacccggaa agagttgccg gctaagggtgg 240
ctaaactacc tccgtcctga tggtagaaga gggaatatta cacccgagga acaacttttg 300
atcatggagc ttcacgcaaa gtggggaaac aggtggtcca aaattgccaa gcatctacct 360
ggtaggacag ataatgagat caagaactat tggaggacca ggatccagaa gcacatcaag 420
caagctgaga actttcagca acaaatacgc aataactctg agataaatga tcaccaagct 480
agcacttagcc atgtttctac catggctgaa cccatggaga cctattctcc acccttttat 540
caaggaatgt tagagccatt ttcttcaatt cagttccccca caattaatcc tgatcaatcc 600

agttgttcta ccaatgacaa caacaacagc attaactatt ggagcatgga ggatatctgg 660
 tcaatgcagt tactgaacgg ggattaaata ttgatataatc aagataaacc taaattcttg 720
 tataagttcc ataaaacact ggaatgtctc tggctaaaa catattatta ttaggtttgt 780
 ttatataagt agttggatat gtttggttt gcgtaccatt attagcatat atatatataat 840
 ttc当地atgag atgctatgtc cattgtaaaa gatatggta agaaccacat agtttcaaaa 900
 ctcttaata taattccagt cacttattat aggaagtcta ttatattat tctccaagat 960
 gtttgcctaa aaaaaaaaaa aaaaaaaaaa 988

<210> 30
 <211> 208
 <212> PRT
 <213> Glycine max

<400> 30
 Met Asp Lys Lys Gln Leu Cys Asn Thr Ser Gln Asp Pro Glu Val Arg
 1 5 10 15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile
 20 25 30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
 35 40 45

Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
 50 55 60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
 65 70 75 80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
 85 90 95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
 100 105 110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
 115 120 125

Ile Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
 130 135 140

Val Ser Thr Met Ala Glu Pro Met Glu Thr Tyr Ser Pro Pro Phe Tyr
 145 150 155 160

Gln Gly Met Leu Glu Pro Phe Ser Ser Ile Gln Phe Pro Thr Ile Asn
 165 170 175

Pro Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Ser Ile Asn
 180 185 190

Tyr Trp Ser Met Glu Asp Ile Trp Ser Met Gln Leu Leu Asn Gly Asp
 195 200 205

<210> 31
 <211> 530
 <212> DNA
 <213> Glycine max

```

<220>
<221> unsure
<222> (301)

<220>
<221> unsure
<222> (356)

<220>
<221> unsure
<222> (388)

<220>
<221> unsure
<222> (393)

<220>
<221> unsure
<222> (470)

<220>
<221> unsure
<222> (485)

<220>
<221> unsure
<222> (495)

<220>
<221> unsure
<222> (513)

<220>
<221> unsure
<222> (517)

<220>
<221> unsure
<222> (522)

<400> 31
aaaataatgg acaagaagct tggcaacacg tctcatgatc ctgaagttag aaaggggcca 60
tggacaatgg aagaagactt aatcttgatc acctatatattt ccaatcacgg ggaagggggtt 120
tggaaactctt tggccaaggc tgctggactt aaacgtaccc gaaagagttt ccggctccgg 180
tggctaaactt acctccgtcc tgatgttaga agagggaaata ttacacccga ggaacagctt 240
ttgatcatgg aacttcatgc aaagtgggaa aacaggtggt ccaaaaattgc caagcatctt 300
nccggaaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacanctca 360
agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420
cttgccacaac caattgtcaa caatgggcaa cccaaaaaaaaa ctaatctcan caatttcaag 480
gaagnttatt cattnaatca attccaaaaa ccncacntct antgtttcaa 530

<210> 32
<211> 204
<212> PRT
<213> Glycine max

<400> 32
Met Asp Lys Lys Leu Gly Asn Thr Ser His Asp Pro Glu Val Arg Lys
    1           5           10          15

```

Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Thr Tyr Ile Ala
20 25 30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
35 40 45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
50 55 60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
65 70 75 80

Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
85 90 95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr
100 105 110

Arg Ile Gln Lys His Leu Lys Gln Ala Ser Ser Ser Phe Gln Gln Gln
115 120 125

Ser Ser Asn Ser Glu Ile Ile Tyr His Pro Gln Ala Cys Thr Ser Gln
130 135 140

Val Ser Thr Met Ala Gln Pro Ile Glu Thr Tyr Ser Pro Pro Ser Tyr
145 150 155 160

Gln Gly Met Leu Asp Pro Phe Ser Ile Gln Phe Pro Thr Asn Pro His
165 170 175

His Ser Ser Cys Cys Thr Asn Asp Asp Asp Asn Asn Asn Tyr Trp Ser
180 185 190

Met Glu Asp Ile Trp Ser Met Gln Leu Ala Asn Tyr
195 200

<210> 33
<211> 910
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (798)

<220>
<221> unsure
<222> (807)

<220>
<221> unsure
<222> (814)

<400> 33
tctctctctca tctctctcta gcgtgcacac aaaataatgg aaaaaaaaaacc atgcgactca 60
tctcatgatc cagaagttag aaagggacca tggatcatgg aagaagactt gatcttgata 120
aactatattt caaatcacgg tgaaggtagtt tggaaattctt tagccaaagc ttctggctt 180
aaacgaacgg gaaagagttg tcgactccgt tggctaaact accttcgtcc tgatgttaga 240
agaggaaaca ttacacccga agaacagctt ttgatcatag aacttcatgc aaagtggggc 300
aataggttgtt caaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360

ttctggagaa ctaggatcca gaagcacatt aagcaagctg agacttcaca acaacatgg 420
aattcatcg agaatagtaa taatgatcat caagcaagca atagcactag caaggtgtcc 480
accatggcac atccaaatga gactttctt tcaccctcat accaagcaac tttttaggcc 540
tttcaacctc aattcctaca atcaatgatc aatcaagttt ttgtaccagg aacaacaact 600
atggagcat cgaggatata tggtcgtcta tgcaattact caatggagat waattaaatc 660
tagctatatg catgctata taaatcatat atgtgatgat atataaacct aagctttat 720
tgagtgtggg caggcttaat aacatcatta ggtctggat atatgagtag gttaagattg 780
gtgtgcgtgc ctaaatgnag tattgcntta ttgnagtaag aataactagt tatggatgcc 840
tttaaaaaaaa agttagttat gaattgaaat atatagtaac ttatatacta aaaaaaaaaa 900
aaaaaaaaaa 910

<210> 34
<211> 206
<212> PRT
<213> Glycine max

<400> 34
Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
1 5 10 15

Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
20 25 30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
35 40 45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
50 55 60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
65 70 75 80

Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
85 90 95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
100 105 110

Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly
115 120 125

Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr
130 135 140

Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro
145 150 155 160

Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser
165 170 175

Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser
180 185 190

Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn
195 200 205

<210> 35
<211> 863
<212> DNA
<213> Glycine max

<400> 35
gcacgagctc tatkacacac acaagtcaat ggataaaaaa caacagtgt a agacgtctca 60
agatcctgaa gtgagaaaag ggccttgac aatggaagaa gacttcatct tcatgaaacta 120
tattgcaaat catggggaaag gtgtttggaa ctcttggcc aaagctgctg gtctcaaacg 180
taacggaaag agttgccgc taaggtggct aaattacctc cgtcctgatg tttagaagagg 240
gaatattaca cccgaggaac aactttgtat tatggagctc cacgcaaat gggaaacag 300
gtgggtccaaa attgccaagc atctacctgg aaggactgtat aatgagatca agaactattg 360
gaggacaagg atccagaagc acatcaagc a gctgagaac tttcagcaac agagtagtaa 420
taattctgaa ataaatgatc accaagctg cactagccat gtttccacca tggctgagcc 480
catggagatg tatttcac cctgttatca aggaatgtt gagccat tttt caactcagtt 540
ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaa tattatcaag 660
ataaaaccta agttypaag ttccataagg ctggaatgtc tytggattaa aacatattat 720
tgggttgtt tatataagta gttggatgtt tggtttgcg taccattt agctatgtgc 780
tgaatataat acgagatyt atattaaact atatctgcat gctttatata taaaaaaaaa 840
aaaaaaaaaaa aaaaaaaaaaaa aaa 863

<210> 36
<211> 206
<212> PRT
<213> Glycine max

<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
1 5 10 15
Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
20 25 30
Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
35 40 45
Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
50 55 60
Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
65 70 75 80
Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
85 90 95
Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
100 105 110
Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
115 120 125
Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
130 135 140
Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr
145 150 155 160
Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro
165 170 175
Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Ile Asn Tyr Trp
180 185 190

Ser	Met	Glu	Asp	Ser	Trp	Ser	Met	Gln	Leu	Leu	Asn	Gly	Asp		
							195	200				205			
<210>	37														
<211>	805														
<212>	DNA														
<213>	Glycine max														
<400>	37														
aaaaaaaccat	gcaactcatc	atctcatgat	cctgaagtga	gaaaggacc	atggaccatg	60									
gaagaagact	tgatcttgc	aaactatatt	gcaaatacag	gtgaaggtgt	ttggactcc	120									
ttagccaaag	cttctggct	caaacgaacg	ggaaagagtt	gtcgactccg	ttggctaaac	180									
tacttcgtc	ctgatgttag	aagagggaaac	attacacccg	aggaacagct	tttgatcata	240									
gaacctcatg	caaagtgggg	caatagggtgg	tccaaaattt	caaagcatct	tccaggaaga	300									
actgacaatg	agattaagaa	cttctggaga	acaaggatcc	aaaagcacat	taagcaagct	360									
gagacttcac	aacaacatgg	taattcagag	aataatgatc	atcaagcaag	cactagtact	420									
agcaaaagtgt	ccaccatggc	acatccaaat	gagactttct	ctccaccctc	ataccaagga	480									
acttttgagc	cattccaacc	tcaattccct	acaatcactg	atcaatcaag	ttgttgtacc	540									
accaccaacg	acaacaacaa	ctattggagc	atcgaggata	tctggtcgtc	tatgcaatta	600									
ctcaatggag	attaaaccta	gctatatgca	tgccatatata	aatcatatat	atgatgatata	660									
ataaacctaa	gctttgttag	agtgtgttca	ggcttaataa	catcattagg	tctgtttata	720									
ttagtagtct	aagtttgggt	tttgaatgc	atgatgtgag	ttaagaatta	attagttat	780									
ggttggaaaaa	aaaaaaaaa	aaaaaa				805									
<210>	38														
<211>	204														
<212>	PRT														
<213>	Glycine max														
<400>	38														
Lys	Lys	Pro	Cys	Asn	Ser	Ser	Ser	His	Asp	Pro	Glu	Val	Arg	Lys	Gly
1				5					10				15		
Pro	Trp	Thr	Met	Glu	Glu	Asp	Leu	Ile	Leu	Ile	Asn	Tyr	Ile	Ala	Asn
			20					25				30			
His	Gly	Gly	Val	Trp	Asn	Ser	Leu	Ala	Lys	Ala	Ser	Gly	Leu	Lys	
			35				40				45				
Arg	Thr	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Leu	Asn	Tyr	Leu	Arg	Pro
			50			55				60					
Asp	Val	Arg	Arg	Gly	Asn	Ile	Thr	Pro	Glu	Glu	Gln	Leu	Leu	Ile	Ile
			65			70			75				80		
Glu	Leu	His	Ala	Lys	Trp	Gly	Asn	Arg	Trp	Ser	Lys	Ile	Ala	Lys	His
			85			90						95			
Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Phe	Trp	Arg	Thr	Arg
			100			105						110			
Ile	Gln	Lys	His	Ile	Lys	Gln	Ala	Glu	Thr	Ser	Gln	Gln	His	Gly	Asn
			115			120						125			
Ser	Glu	Asn	Asn	Asp	His	Gln	Ala	Ser	Thr	Ser	Thr	Ser	Lys	Val	Ser
			130			135						140			
Thr	Met	Ala	His	Pro	Asn	Glu	Thr	Phe	Ser	Pro	Pro	Ser	Tyr	Gln	Gly
			145			150				155			160		

Thr	Phe	Glu	Pro	Phe	Gln	Pro	Gln	Phe	Pro	Thr	Ile	Thr	Asp	Gln	Ser
			165						170					175	
Ser	Cys	Cys	Thr	Thr	Asn	Asp	Asn	Asn	Tyr	Trp	Ser	Ile	Glu		
			180				185				190				
Asp	Ile	Trp	Ser	Ser	Met	Gln	Leu	Leu	Asn	Gly	Asp				
			195				200								
<210>	39														
<211>	751														
<212>	DNA														
<213>	Glycine max														
<400>	39														
tggatgttaa	gaaagggtggg	tctgttagtac	aagcacaagt	gaagttgcag	aagcataacg	60									
aaaaggagat	gggcattgaga	aaagggtccat	gggcgggtga	ggaggacacc	attctggtca	120									
attacatcg	cacacacgg	gaaggccact	ggaattccgt	ggcacgtgt	gcaggtctaa	180									
ggaggagtg	gaagagttgc	agattaaggt	ggctaaacta	cttgcgc	gacgtgcgg	240									
gtggaaat	cacactccaa	gaacaaat	taattctcg	ccttcactct	cgctgggca	300									
acagggtgg	aaagattgt	caacagctgc	caggaagaac	agacaacgaa	ataaagaact	360									
atggaggac	cagagtata	aaacaagcga	agcagctaaa	gtgcgtatgt	aatagcaa	420									
attcagaga	cacgttgcgt	tacgtttg	tgccgcgtt	gctggagcgg	tttcagccc	480									
catcacaagc	actggagcca	aaccaaagt	gacttgtgtt	acacgcttca	tcatcactgc	540									
tcccttcgaa	ttccgaccat	agtattgaaa	gggggtcg	tctgtggca	gtttcaata	600									
accaaatgtt	gttggAACAG	gggagtgccg	gtgacttgtt	ggaaagt	tttg	660									
acaatatgt	cttttgccaa	cagcttctt	atgacctcca	aatgaaataa	aatacaattc	720									
ccttccgtca	cgcaaaaaaaa	aaaaaaaaa	a			751									
<210>	40														
<211>	235														
<212>	PRT														
<213>	Glycine max														
<400>	40														
Asp	Val	Lys	Lys	Gly	Gly	Ser	Val	Val	Gln	Ala	Gln	Val	Lys	Leu	Gln
1				5				10					15		
Lys	His	Asn	Glu	Lys	Glu	Met	Gly	Met	Arg	Lys	Gly	Pro	Trp	Ala	Val
				20				25					30		
Glu	Glu	Asp	Thr	Ile	Leu	Val	Asn	Tyr	Ile	Ala	Thr	His	Gly	Glu	Gly
				35				40				45			
His	Trp	Asn	Ser	Val	Ala	Arg	Cys	Ala	Gly	Leu	Arg	Arg	Ser	Gly	Lys
				50				55				60			
Ser	Cys	Arg	Leu	Arg	Trp	Leu	Asn	Tyr	Leu	Arg	Pro	Asp	Val	Arg	Arg
				65				70				75			80
Gly	Asn	Ile	Thr	Leu	Gln	Glu	Gln	Ile	Leu	Ile	Leu	Asp	Leu	His	Ser
				85				90					95		
Arg	Trp	Gly	Asn	Arg	Trp	Ser	Lys	Ile	Ala	Gln	Gln	Leu	Pro	Gly	Arg
				100				105					110		
Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Arg	Thr	Arg	Val	Ile	Lys	Gln
				115				120				125			

Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr
130 135 140

Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr
145 150 155 160

Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser
165 170 175

Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser
180 185 190

Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser
195 200 205

Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe
210 215 220

Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys
225 230 235

<210> 41

<211> 500

<212> DNA

<213> Glycine max

<400> 41

catttctaat tgttctgatc catatatatac atactttctt tgtaataact taaagaaccc 60
cacaaaaaaca ccaaccatgt ccacaatgc aaagagagat ttgagttcta atgaagaaga 120
gagttagctg agaagaggtc ctggactct tgaagaagac agcttactca tacactatat 180
tgctcgcat ggtgaaggcc gttggatat gttagccaaa agtgcaggat tgaagaggac 240
tggaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300
cctcaactcca caggagcaac tcttgatccct tgaactccat tccaagtggg gtaacaggtg 360
gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420
aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480
ttgatgctgt cagtgtttt 500

<210> 42

<211> 229

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (138)

<400> 42

Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Ser
1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile
20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys
35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu
65 70 75 80

Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser
85 90 95

Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
100 105 110

Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu
115 120 125

Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro
130 135 140

Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His
145 150 155 160

Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser
165 170 175

Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser
180 185 190

Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His
195 200 205

Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro
210 215 220

Ile Phe Thr Ala Thr
225

<210> 43
<211> 1348
<212> DNA
<213> Glycine max

<400> 43
tacctctcca accaagacca atttgaaaac ctcttcaatc caacaacaa acgttctccc 60
tttgttctg agagaatcaa tggatggaaa aggagcaaga agtagcaaca cccttttaag 120
tagtgaggac gagatggacc ttgcgaagagg cccttggacc gtcgatgaag acctcaactct 180
tatcaattac gttgcactc atggcgaagg tcgctgaaat accctcgccc totctgctgg 240
gctgaaacga acgggaaaga gttgcagatt gaggtggctg aattatctgc gtcctgatgt 300
tcgacgtgga aacatcacgc ttgaagaaca acttttgatt ctggagctcc attctcgctg 360
ggaaaccga tggtcaaaaa ttgctcaata tttgcctggt agaaccgaca atgagataaa 420
gaactattgg agaacccgtg tccaaaagca tgccaaagcaa ctcaaattgcg acgtgaataag 480
caagcaattc aaggacacca tgcgttacat ttggatgcca aggctgtgg aacgcattca 540
agccaccgct gccgcctccg caccacaacc cgtaaccgtt ccaccgcgac caacaatgca 600
tacacctacg gaagcaacct taataacaac aaattcgagg ttacacgatca caagggcaaa 660
atggggttaa ccgatccctc agttatgaac aatgacttaa tgggttcaca tgtcacgcaa 720
agttacaccc ctgagaatag tagcaccggt gcgtcatcat cagactcggt tggactcaa 780
gtctcagcaa tttctgattt gactgaatat tacactgtca ctggtagtgg taacaataac 840
aatactaatt ctgcggatta ttatcaaccc tctcaaattt gttactcgga tagttgcattc 900
acaagcccat ctgggttgg ccctcaaggg ctgatatttc aatccatgga tccaaacacc 960
ccgtggaaca tgcaaagtgg ggactcctt gacagtttt ggaacgttga aagcatgtt 1020
ttcttagagc agcaactcat gaatgacaac atgtgaaaac attgggata gggaaaataag 1080
acttagatac gttcttctt agtattgtt ttaattaaa gttaaagttt acacaagttt 1140
ttgaagtgaa actttaattt taattgaata ataatactga aaacaagagt tttatTTTaa 1200
tttattctt ttatgaatta tgaatttagt tgacagaagg gttgtttgtt gaaatataaca 1260

ggtgaaaagta tagaaaggtag caacattaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1348

<210> 44
<211> 196
<212> PRT
<213> Glycine max

<400> 44
Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu
1 5 10 15

Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
20 25 30

Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr
35 40 45

Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
50 55 60

Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
65 70 75 80

Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
85 90 95

Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
100 105 110

Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
115 120 125

Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile
130 135 140

Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser
145 150 155 160

Ala Pro Gln Pro Val Thr Val Pro Pro Arg Pro Thr Met His Thr Pro
165 170 175

Thr Glu Ala Thr Leu Ile Thr Thr Asn Ser Arg Phe Thr Ile Thr Arg
180 185 190

Ala Lys Trp Gly
195

<210> 45
<211> 1236
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (519)

<220>
<221> unsure
<222> (521)

```

<220>
<221> unsure
<222> (530)..(531)

<220>
<221> unsure
<222> (534)

<220>
<221> unsure
<222> (800)

<220>
<221> unsure
<222> (1124)

<220>
<221> unsure
<222> (1151)

<400> 45
aacaatccaa ctcttttct ccctatccca acaatctcac tcatacctct tcaatctaac   60
aaacttaatt tctttgttt tgagtttctt agagaatgga tgaaaaaggaa gcaagaagta 120
gcaacaccct tttaagtgtt gaggacgaga tggaccttcg aagaggccct tggaccgtcg 180
atgaagacct cacttttac aattacatttgc ccactcatgg cgaaggtcgc tggaaacacgc 240
tcgcctctc tgctgggctg aaacgaacgg ggaagagttt cagattgagg tggctgaatt 300
atctgcgtcc tgatgttca cgtggaaaca tcacacttga agaacaactt ttgattctgg 360
agtttatttc tcgctgggaa aaccgttggt cgaaaatttgc tcaatatttgc cctggtagaa 420
ccgacaacga gataaaagaac tattggagaa cccgtgtcca aaagcatgcc aagcaactca 480
aatgtgacgt gaatagcaag caattcaagg acaccatngt ntaccttgn natnccaagg 540
ctcggtggaaac gcattcaagc agcggcgacg gccccctgaa ccaccaccgt aactgcggcc 600
gcacccaaca atgcatttac ctacggrraac aaccttatac caccaatttgc gagggtctga 660
atcacaaggc cagaatgggg ttaaccgtatc cttcagttgc gaacaatgac tttgtgggtt 720
cacatgtcac gcaaaggatc cctactcttgc agaatagtagt cacgggtgcg tcatcatcag 780
actcggttgg gactcaagtn tcaacaattt ctgatttgc tggaaatttcc agtgcggcc 840
aaaataactaa ttctgcggat tattatcaac cctctcaaat tagtaatttgc tggataatt 900
gcatcacaag cccatctggg ttcttgttcc ctcaaggact agatcttcaa tccatggatc 960
caaacacacc gtggAACATG caaagtgggg actcctcttgc caatttttgg gacgttgaaa 1020
gcatgttatt cttagagcag caactcatgttgc atgacaacat gtggaaacatttggaaatagga 1080
aaaataagact tagatacggt tcttcttaata ttttttagtgc tgngttta attaaagtttgc 1140
aagttaacac nagttatttgc agtggaaactt taattttaat taaataataa tcctgaaaaaa 1200
aaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa 1236

<210> 46
<211> 322
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (142)

<220>
<221> UNSURE
<222> (145)..(146)..(147)

<220>
<221> UNSURE
<222> (178)

```

<400> 46
 Met Asp Glu Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Cys Glu
 1 5 10 15
 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
 20 25 30
 Thr Leu Ile Asn Tyr Ile Ala Thr His Gly Glu Gly Arg Trp Asn Thr
 35 40 45
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
 50 55 60
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
 65 70 75 80
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
 85 90 95
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
 100 105 110
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
 115 120 125
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Xaa Tyr Leu
 130 135 140
 Xaa Xaa Xaa Lys Ala Arg Gly Thr His Ser Ser Ser Gly Asp Gly Pro
 145 150 155 160
 Arg Asn His His Arg Asn Cys Gly Arg His Gln Gln Cys Ile His Leu
 165 170 175
 Arg Xaa Gln Pro Tyr Thr Thr Lys Phe Glu Val Leu Asn His Lys Gly
 180 185 190
 Arg Met Gly Leu Thr Asp Pro Ser Val Ala Asn Asn Asp Phe Val Gly
 195 200 205
 Ser His Val Thr Gln Arg Tyr Pro Thr Pro Glu Asn Ser Ser Thr Gly
 210 215 220
 Ala Ser Ser Ser Asp Ser Phe Gly Thr Gln Val Ser Thr Ile Ser Asp
 225 230 235 240
 Leu Thr Glu Asn Ser Ser Val Pro Glu Asn Thr Asn Ser Ala Asp Tyr
 245 250 255
 Tyr Gln Pro Ser Gln Ile Ser Asn Tyr Ser Asp Asn Cys Ile Thr Ser
 260 265 270
 Pro Ser Gly Phe Leu Phe Pro Gln Gly Leu Asp Leu Gln Ser Met Asp
 275 280 285
 Pro Asn Thr Pro Trp Asn Met Gln Ser Gly Asp Ser Ser Asp Asn Phe
 290 295 300

Trp Asp Val Glu Ser Met Leu Phe Leu Glu Gln Gln Leu Met Asn Asp
305 310 315 320

Asn Met

<210> 47
<211> 1181
<212> DNA
<213> Glycine max

<400> 47
tttcagttag tgagaatagc catgtctact tcaaagagcg tcagcagtgc tagtgaagat 60
gacaatgaac tttagaaggagg gccttgact ctggaagagg ataacttgct ctcccaatat 120
attttaatc atggggaaagg gcgatggaat ttgctggcta aacgttcagg attaaagaga 180
actggggaaaa gttcagatt aaggtggcta aattatctaa agccagatgt aaaacgggga 240
aatttaacc cacaagagca acttataatt ctgaaactcc actcaaagtg gggaaacagg 300
tggtcaaaaa ttgcacaaca tttgccagggc agaacagaca atgaaatcaa gaactattgg 360
agaacttagga ttcaaaaaca agcaagacat ttgaaaattt acactgacag cagagagtt 420
caagaacttg ttaggcgttt ctggatgcct agattgcctc agaaaagcaaa agaattcatct 480
tcctcaaaaca tgtcaattca aaaccaggca attcctatgc ctttgatta tgtttctcag 540
catttaactg ttgggaccat acctccttgg cagggacctt gtatgaatga agctggccc 600
acttacatgg accaacatga gcagactcag actcggaaaca ccaacaatgg ttcatgcattc 660
tccttgcctg agtcagcaaa tattccaaaa gtgcctcagc attttggaca caccaccatc 720
acccaatttc atgccttgaa taccaatgac tttggcacct tcacatatga aggttataat 780
gtaaaacaaca atgtctatga gatggacaac ttcaaaaacga ctactacatg ggtggctgag 840
gatgcgcaat acccaatttg tgattgtcaa atgtaggaa gcaattgggt aaacaacgat 900
tttgcattgt acatgtggaa catggatgaa ctgtggcagt tttagcaagtt acaaaaataa 960
gatttttaggg tttttttttt ttttggataaa ccaaaaagtcc aaaactctt ctttgatgac 1020
gttattattt ttagtcatgaa ctgtggatta gctaccgaat taattaatac agatggcgat 1080
tgttttctgt acatctgtct ttttgcattgt ttttgcattgt acaaaaataa 1140
tgattgagaa aagtcaattaa tttagtcaacta gtacaaaaaa a 1181

<210> 48
<211> 312
<212> PRT
<213> Glycine max

<400> 48
Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
1 5 10 15

Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
20 25 30

Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
35 40 45

Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
50 55 60

Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
65 70 75 80

Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
85 90 95

Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr
 115 120 125
 Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
 130 135 140
 Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Asn Met Ser Ile Gln
 145 150 155 160
 Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr
 165 170 175
 Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly
 180 185 190
 Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn
 195 200 205
 Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val
 210 215 220
 Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn
 225 230 235 240
 Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn
 245 250 255
 Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Trp Val Ala
 260 265 270
 Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn
 275 280 285
 Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu
 290 295 300
 Trp Gln Phe Ser Lys Leu Gln Lys
 305 310
 <210> 49
 <211> 1186
 <212> DNA
 <213> Glycine max
 <400> 49
 aattcggcac gaggccatgt ctacttcaaa gagcgtcagc agttcttagtg aagatgacaa 60
 tgaacttaga agagggcctt ggactcttga agaggataat ttgcctccc aatatatttc 120
 tagtcatgga gaagggcgat ggaatttgc agctaaacgt tcaggattaa agcgaactgg 180
 gaaaagtgc agattaaggt gcctaatttca tctaaagcca gatgtaaaac gggaaatttt 240
 aaccccaacaa gagcaactta taatcctcga actccactca aagtggggaa acaggtggtc 300
 aaaaattgca caaaatttgc caggcagaac agacaatgaa atcaagaact attggagaac 360
 tagattcag aaacaagcaa gacatttgc aattgacact gacaccagag agtttcagga 420
 acttgtttagg cgtttcttgc tgccatgttgc cttcaaaaag cccaaatc atcttcttca 480
 gccatgtcaa ttcaaaaacca ggcaactcct atgccttttgc atgggttttc tcagcattca 540
 actgttggga ccataccatc acattcacac accccttgc agggaccccttgc tatgaatgaa 600
 gctgggtccca cttacatgga ccaacatgag cagaactcag actctgaaca caacaatgg 660
 tcatgcatttgc ctttgcgttgc gtcagcaat tttccaaaag tgccctcagca ttttggacgc 720
 accaccatca cccaaatatca tgcccttgc aacaatgact ttggcacctt cacatatgac 780
 ggctacaatg taagcaacaa tgtctatgag atggacaact tcaaaaacgcc tactacaagg 840
 gtggctgagg atgcgcaata cccaaatgttgc gattgtcaaa tggtaggaag caattgggttca 900

aacagcgatt ttgcatgtaa catgtggAAC atggatgaat tgtggcaatt tagcaaggta 960
caaaaataag atttttagggt ttggTTTTT tggagttacc aagactctat ctttgggtat 1020
gttattattt gttatcatgaa ctgttgattt gctactacca aattaattaa tacagatgtt 1080
gattgttttc tgtacatctg ttttgcattt ctctgtttt caatttgtat tgattgagaa 1140
aagtcatcaa ttagtcacta gttcaaaaca caaaaaaaaaaaaaaa aaaaaaaaaa 1186

<210> 50
<211> 192
<212> PRT
<213> Glycine max

<400> 50
Met Ser Thr Ser Lys Ser Val Ser Ser Ser Glu Asp Asp Asn Glu
1 5 10 15

Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
20 25 30

Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
35 40 45

Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
50 55 60

Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
65 70 75 80

Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
85 90 95

Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Asp Thr
115 120 125

Asp Thr Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
130 135 140

Cys Phe Lys Lys Pro Lys Asn His Leu Leu Gln Pro Cys Gln Phe Lys
145 150 155 160

Thr Arg Gln Leu Leu Cys Leu Leu Met Val Phe Leu Ser Ile Gln Leu
165 170 175

Leu Gly Pro Tyr His His Ile His Thr Pro Leu Gly Arg Asp Leu Val
180 185 190

<210> 51
<211> 487
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (358)

<220>
<221> unsure
<222> (429)

<400> 51
gagaaaataaa aagagaagaa agaaaaacacg atagtatcat catatcacca ccacacacat 60
agatagagag aggaaaaacga cctatatattt ttttcctttg agagcttcag gggcttaggaa 120
aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180
acatgggaag accaccttg ttttatattt aaggggtcaa gaaagggcct tggactcctg 240
aagaagacat catattggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300
ttcctgccaa aacagggtt tcaagatgca gcaagagttt cagacttaga tggacgantt 360
acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420
cattttcang atcttttagg aaacagatgg ggtgcaatag ctccataacct tccacaaagg 480
acaaggg 487

<210> 52
<211> 90
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (59)

<220>
<221> UNSURE
<222> (72)

<220>
<221> UNSURE
<222> (83)

<400> 52
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
20 25 30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly
50 55 60

Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile
65 70 75 80

His Leu Xaa Asp Leu Leu Gly Asn Arg Trp
85 90

<210> 53
<211> 1556
<212> DNA
<213> Glycine max

<400> 53
gcacgaggag aaataaaaag agaagaaaaga aaacacgata gtatcatcat atcaccacca 60
cacacataga tagagagagg aaaacgacct atatttttt tccttgaga gtttcagggg 120
ctaggaaaat tagaaggaca gccacaagta taaaggcggt gaaataaaag agaaagacaa 180
gaaggagaca tggaaagacc accttggttgt gacaaagaag gggtcaagaa agggccttgg 240
actcctgaag aagacatcat attgggtgtct tatattcagg aacatgtcc tgaaaattgg 300
aggcagttc ctgccaaac agggttgtca agatgcagca agagttgcag acttagatgg 360

acgaattacc	tgagggcagg	aatcaagcgt	ggtaacttca	cagaacaaga	ggagaagatg	420
ataatccatc	ttcaagatct	tttagaaaac	agatgggctg	caatacgctc	ataccttcca	480
caaagaacag	acaatgacat	aaagaactat	tgaatacc	atttgagaaa	gaagctgaag	540
aagatgcaag	cagggcgtga	aggtggtagc	tttggagaag	ggtttcagc	ctcaaggcaa	600
atccctagag	gccagtggg	aagaaggctc	caaactgata	tccaaatggc	aaagagagcc	660
ctcagtgaag	ctcttcacc	agagaaaaag	ccatcttgtt	tatctgcctc	aaactcaaac	720
ccttcagata	gtacgagtc	cttcttcc	acaaaaccaa	caacaacaca	atctgtgtgc	780
tatgcataa	gtgctgacaa	catagctaga	atgctcaagg	gttggatgaa	gaacccacca	840
aagtccctcaa	gaaccaactc	gtctatgact	cagaactcat	tcaacaactt	agcaggtgct	900
gatactgctt	gtagtagtgg	agcaaaggga	ccactaagca	gtgccaatt	gtctgagaat	960
aattttgaat	ccttgggtga	tttgatcag	tcttggagt	cttcaaactc	tgatcaattc	1020
tctcagtcct	tgtctcctga	ggccactgtt	ttgcaagatg	aaagcaagcc	tgatattaat	1080
attgctgcag	aaattatgcc	cttctcttg	cttgagaaat	ggctccttga	tgagggcaggt	1140
tgccaagaga	aatttagttgg	ttgttgttgt	gatgccaagt	ttttctaagt	ttgggttcatt	1200
tttgacata	tgagactgtg	ggatttttt	attttatttt	attttatttc	ataagttata	1260
ggtagggcct	catcaattaa	tctcgcttcg	gccttattag	agagagaagt	tttccagcct	1320
ttgggtctag	acgtgtatat	gttaattatt	attgacatta	tgatgattat	tatcatactg	1380
tgttagttgc	cataactgg	caaacttgc	tctcttatgt	aaagttgatc	ttgcgacgag	1440
atccctgttt	atggctttag	gcagcgcgac	cggtcttc	tctttgtgc	gcttgattag	1500
taacccccc	cggggggggc	ccgggtccaa	atcccccta	atgggtcct	ttttag	1556

<210> 54
<211> 332
<212> PRT
<213> Glycine max

<400> 54
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
20 25 30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Lys Met Ile Ile His
65 70 75 80

Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
85 90 95

Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
100 105 110

Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Ser Phe
115 120 125

Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
130 135 140

Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
145 150 155 160

Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
165 170 175

Asn Pro Ser Asp Ser Ser Ser Phe Ser Ser Thr Lys Pro Thr Thr
 180 185 190
 Thr Gln Ser Val Cys Tyr Ala Ser Ser Ala Asp Asn Ile Ala Arg Met
 195 200 205
 Leu Lys Gly Trp Met Lys Asn Pro Pro Lys Ser Ser Arg Thr Asn Ser
 210 215 220
 Ser Met Thr Gln Asn Ser Phe Asn Asn Leu Ala Gly Ala Asp Thr Ala
 225 230 235 240
 Cys Ser Ser Gly Ala Lys Gly Pro Leu Ser Ser Ala Glu Leu Ser Glu
 245 250 255
 Asn Asn Phe Glu Ser Leu Phe Asp Phe Asp Gln Ser Leu Glu Ser Ser
 260 265 270
 Asn Ser Asp Gln Phe Ser Gln Ser Leu Ser Pro Glu Ala Thr Val Leu
 275 280 285
 Gln Asp Glu Ser Lys Pro Asp Ile Asn Ile Ala Ala Glu Ile Met Pro
 290 295 300
 Phe Ser Leu Leu Glu Lys Trp Leu Leu Asp Glu Ala Gly Cys Gln Glu
 305 310 315 320
 Lys Leu Val Gly Cys Cys Gly Asp Ala Lys Phe Phe
 325 330
 <210> 55
 <211> 357
 <212> DNA
 <213> Triticum aestivum
 <220>
 <221> unsure
 <222> (259)
 <220>
 <221> unsure
 <222> (307)
 <220>
 <221> unsure
 <222> (319)
 <400> 55
 gccaaagtat caggttttag ggggtggggga tccaaaaatt aggttagctat attgaagtat 60
 tttgcgcaaa gtcgcaacaa caaatgtcac cttagtcaat aactttcttc ttgcttcaac 120
 ctctgtatac tccatgcagg cctcaaccgc acaggaaaga gctgtcgccct ccgggtgggtt 180
 aactaacctcc acccttgggcc taaagcgtgg ggcgcattgact ccccatgaaa gaacgcctca 240
 tcctccaact ccatgctcng tggggaaaca agtgtccaa ggataaacacg gaactgccaa 300
 ggcgtancga caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357
 <210> 56
 <211> 54
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (21)

<220>
 <221> UNSURE
 <222> (27) .. (28)

<220>
 <221> UNSURE
 <222> (41)

<400> 56
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15

Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu
 20 25 30

Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys
 35 40 45

Asp Asn Thr Glu Leu Pro
 50

<210> 57
 <211> 1072
 <212> DNA
 <213> *Triticum aestivum*

<400> 57
 gcacgaggcc aaagtatca gtttggggatcc aaaaatttgg tagctataatt 60
 gaagtatttt gcgcaaagtc gcaacaacaa atgtcacctt tgctaataac tttcttcttg 120
 cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtgcctccg 180
 gtgggttaac tacctccacc ctggcctaaa gcgtgggcgc atgactcccc atgaagaacg 240
 cctcatcctc gagctccatg ctgcgtgggg aaacaggtgg tccaggatag cacggaagct 300
 gccaggcgat accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360
 acaggagagg aagaggagcg tgcaccctc accatcttca tcctcagtga cataccaatc 420
 cattcagccca cagacccat cgatcatggg aattggcgag caggaacttc atggtggcag 480
 tagctgcatac acaagcatat tgaaggcac gcctgctgac atggatggat acctcatgga 540
 tcagatatgg atggagattt aggcaccctc tgggtcaac tttcatgacg ggaaggataa 600
 ttcatacagc agccctctg gccctctgct gccatcaccg atgtgggatt actacagccc 660
 tgaggcaggc tggaaatgg atgagataaa gatggccca caagtttagt acagtaaagg 720
 aattggccca agttattgaa gccatatata ttgtatcaga ttactaagtt acttgcaacc 780
 tagcagaagt gaaatgcttt tggtaaaa accattagca tggatctaaa aaatatttat 840
 atctatctag cattccaagt gtgctcatgt tttatgtatc tactatgtatc catctagtgt 900
 gcaagacatg taatgcaagg acactccac tttgtattca caataatcag ctatctccctg 960
 taagactttt ccaatgcaaaa catgattagc aggtgtaata tcaactaaa tgctgccaa 1020
 aaaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aaaaaaaaaaaaa aa 1072

<210> 58
 <211> 198
 <212> PRT
 <213> *Triticum aestivum*

<400> 58
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu
 20 25 30

 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg
 35 40 45

 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 50 55 60

 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val
 65 70 75 80

 Ser Pro Ser Pro Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro
 85 90 95

 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly
 100 105 110

 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp
 115 120 125

 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly
 130 135 140

 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly
 145 150 155 160

 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly
 165 170 175

 Trp Lys Met Asp Glu Ile Lys Met Ala Pro Gln Val Ser Tyr Ser Lys
 180 185 190

 Gly Ile Gly Pro Ser Tyr
 195

 <210> 59
 <211> 521
 <212> DNA
 <213> Triticum aestivum

 <220>
 <221> unsure
 <222> (108)

 <220>
 <221> unsure
 <222> (355)

 <220>
 <221> unsure
 <222> (361)

 <220>
 <221> unsure
 <222> (392)

 <220>
 <221> unsure
 <222> (414)

```

<220>
<221> unsure
<222> (431)

<220>
<221> unsure
<222> (434)

<220>
<221> unsure
<222> (447)

<220>
<221> unsure
<222> (456)

<220>
<221> unsure
<222> (459)

<400> 59
cttggatcc ccactagcta cgtcgtccat gcatgtggtg ctgcagagtc gtagcagcaa 60
cagcatggcg gcggagccgg aggaggaggc ggaccggagg aggaggcngg agctccggcg 120
agggccgtgg acgggtggacg aggacctac gctgatcaac tacatcgccg accacggcg 180
ggcccgctgg aacgcgctgg cgcggccgc cggcctgagg cgcacggga agagctgccg 240
gctgcgtgg ctgaactacc tccgccccga cgtgaagcgc ggcaacttca cccggcggaca 300
gcagctccctc atcctcgacc tccactctcg ctggggcaac cggtggtcga agatngcgc 360
ncacctcccg ggtcgacgg acaacgaaga tnaaagaact actgggagga ccanggtgca 420
aaaagcacgc naancaactc aactgcnaac tccggnaanc gcaaccctta aaggatgcca 480
ataaggtacc tctggatgcc tcgcctctca acgcatcaac c 521

<210> 60
<211> 131
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (27)

<220>
<221> UNSURE
<222> (109)

<220>
<221> UNSURE
<222> (111)

<220>
<221> UNSURE
<222> (122)

<220>
<221> UNSURE
<222> (129)

<400> 60
Met Asp Val Val Leu Gln Ser Arg Ser Ser Asn Ser Met Ala Ala Glu
    1          5           10          15

```

Pro Glu Glu Glu Ala Asp Arg Arg Arg Arg Xaa Glu Leu Arg Arg Gly
20 25 30

Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp
35 40 45

His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg
50 55 60

Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
65 70 75 80

Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu
85 90 95

Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His
100 105 110

Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr
115 120 125

Xaa Val Gln
130

<210> 61
<211> 464
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (435)

<220>
<221> unsure
<222> (442)

<220>
<221> unsure
<222> (450)

<220>
<221> unsure
<222> (457)

<400> 61
acggggcgag acgtgagcat ggggaggccc ccgtgctgcg acaaggaggg cgtcaagaag 60
ggcccttggg cgccggagga ggacctcggt ctctgtctcct acgtccagga gcaacggcccc 120
ggcaactggc gcgcgggtccc caccaggacc ggctgtatgc ggtgttagcaa gagctgccgg 180
ctccgggtggg ccaactacact ggcggccaggg atcaaggcgcg gcaacttcac cgaccaggag 240
gagaagctca tcgttccacct ccaggcgctg ctccggcaaca ggtggggccgc gatcgctcc 300
tacctccccg agcgcaccga caacgacatc aagaactact ggaacacgca actcaagcgc 360
aagctgcaag cggggggcga cgccgcggc aaaccggcg 420
aaagggaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62
<211> 122
<212> PRT
<213> Triticum aestivum

<400> 62
 Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1 5 10 15

 Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His
 20 25 30

 Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg
 35 40 45

 Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

 Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His
 65 70 75 80

 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95

 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu
 100 105 110

 Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala
 115 120

 <210> 63
 <211> 217
 <212> PRT
 <213> Pisum sativum

 <400> 63
 Met Asp Lys Lys Pro Cys Asn Ser Ser Gln Asp Pro Glu Val Arg Lys
 1 5 10 15

 Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
 20 25 30

 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
 35 40 45

 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50 55 60

 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
 65 70 75 80

 Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
 85 90 95

 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
 100 105 110

 Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn
 115 120 125

 Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His
 130 135 140

Pro His Gln Pro Ser Ser Ser Gln Val Ser Asn Leu Val Glu Pro Met
145 150 155 160

Glu Thr Tyr Ser Pro Thr Ser Tyr Gln Gly Thr Leu Glu Pro Phe Pro
165 170 175

Thr Gln Phe Pro Thr Ile Asn Asn Asp His His Gln Asn Ser Asn Cys
180 185 190

Cys Ala Asn Asp Asn Asn Asn Asn Tyr Trp Ser Met Glu Asp Ile
195 . 200 205

Trp Ser Met Gln Leu Leu Asn Gly Asp
210 215